NO:2), especially a coding sequence shown in Figure 3 (SEQ ID NO:1). A preferred *gai* mutant lacks part or all of the 17 amino acid sequence underlined in Figure 4.

C1 cont

Please replace the paragraph beginning at page 10, line 10, with the following rewritten paragraph:

C2 Since the GAI amino acid sequence of Arabidopsis shown in Figure 4 (SEQ ID NO:2) includes 5 consecutive histidines close to its N-terminus, substantial purification of GAI or gai may be achieved using Ni-NTA resin available from QIAGEN Inc. (USA) and DIAGEN GmbH (Germany). See Janknecht et al[31] and EP-A-0253303 and EP-A-0282042. Ni-NTA resin has high affinity for proteins wiht consecutive histidines close to the N- or C-terminus of the protein and so may be used to purifiy GAI or gai proteins from plants, plant parts or extracts or from recombinant organisms such as yeast or bacteria, e.g. *E. coli*, expressing the protein.

Please replace the paragraph beginning at page 11, line 18, with the following rewritten paragraph:

C3 Antibodies raised to a GAI, or gai, polypeptide can be used in the identification and/or isolation of homologous

polypeptides, and then the encoding genes. Thus, the present invention provides a method of identifying or isolating a polypeptide with GAI function or ability to confer a *gai* mutant phenotype, comprising screening candidate polypeptides with a polypeptide comprising the antigen-binding domain of an antibody (for example whole antibody or a fragment thereof) which is able to bind an *Arabidopsis* GAI or gai polypeptide, or preferably has binding specificity for such a polypeptide, such as having the amino acid sequence shown in Figure 4 (SEQ ID NO:2).

Please replace the paragraph beginning at page 12, line 19, with the following rewritten paragraph:

A further aspect of the present invention provides a method of identifying and cloning GAI homologues from plant species other than *Arabidopsis thaliana* which method employs a nucleotide sequence derived from that shown in Figure 3 (SEQ ID NO:1). Sequences derived from these may themselves be used in identifying and in cloning other sequences. The nucleotide sequence information provided herein, or any part thereof, may be used in a data-base search to find homologous sequences, expression products of which can be tested for *GAI* function. Alternatively,

C4 Cont. nucleic acid libraries may be screened using techniques well known to those skilled in the art and homologous sequences thereby identified then tested.

Please replace the paragraphs beginning at page 13, line 14, with the following rewritten paragraphs:

C5 In a preferred embodiment of this aspect of the present invention, the nucleic acid used for probing of candidate nucleic acid encodes an amino acid sequence shown in Figure 4 (SEQ ID NO:2), a sequence complementary to a coding sequence, or a fragment of any of these, most preferably comprising a nucleotide sequence shown in Figure 3 (SEQ ID NO:1).

Alternatively, as discussed, a probe may be designed using amino acid sequence information obtained by sequencing a polypeptide identified as being able to be bound by an antigen-binding domain of an antibody which is able to bind a GAI or gai polypeptide such as one with the amino acid sequence shown in Figure 4 (SEQ ID NO:2).

Please replace the paragraph beginning at page 14, line 21, with the following rewritten paragraph:

The present invention also extends to nucleic acid encoding a *GAI* homologue obtained using a nucleotide sequence derived from that shown in Figure 3 (SEQ ID NO:1).

Please replace the paragraph beginning at page 15, line 1, with the following rewritten paragraph:

Homology may be at the nucleotide sequence and/or amino acid sequence level. Preferably, the nucleic acid and/or amino acid sequence shares homology with the sequence encoded by the nucleotide sequence of Figure 3 (SEQ ID NO:1), preferably at least about 50%, or 60%, or 70%, or 80% homology, most preferably at least 90% or 95% homology. Nuleic acid encoding such a polypeptide may preferably share with the *Arabidopsis thaliana GAI* gene the ability to confer a particular phenotype on expression in a plant, preferably a phenotype which is GA responsive (i.e. there is a change in a characteristic of the plant on treatment with GA), such as the ability to inhibit plant growth where the inhibition is antagonised by GA. As noted, *GAI* expression in a plant may affect one or more other characteristics of the plant. A preferred characteristic that may be shared with the *Arabidopsis thaliana GAI* gene is the ability to complement a *GAI* null mutant phenotype in

C7 cont a plant such as *Arabidopsis thaliana*, such phenotype being resistance to the dwarfing effect of paclobutrazol.

Please replace the paragraphs beginning at page 16, line 3, with the following rewritten paragraphs:

As is well-understood, homology at the amino acid level is generally in terms of amino acid similarity or identity. Similarity allows for "conservative variation", i.e. substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or

C8 glutamine for asparagine. Similarity may be as defined and determined by the TBLASTN program, of Altschul et al. (1990) *J. Mol. Biol.* 215: 403-10, which is in standard use in the art. Homology may be over the full-length of the GAI sequence of Figure 4 (SEQ ID NO:2), or may more preferably be over a contiguous sequence of 17 amino acids, compared with the 17 amino acids underlined in Figure 4, or a longer sequence, e.g. about 20, 25, 30, 40, 50 or more amino acids, compared with the amino acid sequence of Figure 4 (SEQ ID NO:2) and preferably including the underlined 17 amino acids.

C8 cont

At the nucleic acid level, homology may be over the full-length or more preferably by comparison with the 51 nucleotide coding sequence within the sequence of Figure 3 (SEQ ID NO:1) and encoding the 17 amino acid sequence underlined in Figure 4, or a longer sequence, e.g. about, 60, 70, 80, 90, 100, 120, 150 or more nucleotides and preferably includeing the 51 nucleotide of Figure 3 (SEQ ID NO:1) which encodes the underlined 17 amino acid sequence of Figure 4.

Please replace the paragraph beginning at page 17, line 16, with the following rewritten paragraph:

C9

A further aspect of the present invention provides a nucleic acid isolate having a nucleotide sequence encoding a polypeptide which includes an amino acid sequence which is a mutant, allele, derivative or variant sequence of the GAI amino acid sequence of the species *Arabidopsis thaliana* shown in Figure 4 (SEQ ID NO:2), or is a homologue of another species or a mutant, allele, derivative or variant thereof, wherein said mutant, allele, derivative, variant or homologue differs from the amino acid sequence shown in Figure 4 (SEQ ID NO:2) by way of insertion, deletion, addition and/or substitution of one or more amino acids, as

obtainable by producing transgenic plants by transforming plants which have a *GAI* null mutant phenotype, which phenotype is resistance to the dwarfing effect of paclobutrazol, with test nucleic acid, causing or allowing expression from test nucleic acid within the transgenic plants, screening the transgenic plants for those exhibiting complementation of the *GAI* null mutant phenotype to identify test nucleic acid able to complement the GAI null mutant, deleting from nucleic acid so identified as being able to complement the *GAI* null mutant a nucleotide sequence encoding the 17 amino acid sequence underlined in Figure 4 or a contiguous 17 amino acid sequence in which at least 10 residues have similarity or identity with the respective amino acid in the corresponding position in the 17 amino acid sequence underlined in Figure 4, more preferably 11, 12, 13, 14, 15, 16 or 17.

Please replace the paragraphs beginning at page 34, line 3, with the following rewritten paragraphs:

Figure 3: A nucleotide sequence of (SEQ ID NO:1) a *GAI* gene encoding a polypeptide with GAI function.

Figure 4: Primary structure of GAI and gai proteins. The amino acid sequence (SEQ ID NO:2) predicted from the genomic DNA sequence of GAI is shown. The 17 amino acid segment deleted in gai is shown in bold face and double-underlined.

Please replace the paragraphs beginning at page 34, line 14, with the following rewritten paragraphs:

Figure 6a: Nucleotide sequence of *gai-d1* (SEQ ID NO:3).

Figure 6b: Amino acid sequence of *gai-d1* (SEQ ID NO:4).

Figure 6c: Nucleotide sequence of *gai-d2* (SEQ ID NO:5).

Figure 6d: Amino acid sequence of *gai-d2* (SEQ ID NO:6).

Figure 6e: Nucleotide sequence of *gai-d5* (SEQ ID NO:7).

Figure 6f: Amino acid sequence of *gai-d5* (SEQ ID NO:8).

C11 cont

Figure 6g: Nucleotide sequence of *gai-d7* (SEQ ID NO:9).

Figure 6h: Amino acid sequence of *gai-d7* (SEQ ID NO:10).

Please replace the paragraphs beginning at page 37, line 21, with the following rewritten paragraphs:

C12

Primer N6 (SEQ ID NO:11): 5'TAG AAG TGG TAG TGG3';

Primer AT1 (SEQ ID NO:12): 5'ACC ATG AGA CCA GCC G3'.

Please replace the paragraph beginning at page 38, line 19, with the following rewritten paragraph:

C13

Searches of the DNA and protein sequence databases revealed no domains of obvious functional significance within GAI. *gai* contains a deletion of 51 bp from within the *GAI* ORF. This in-frame deletion results in the absence, in gai, of a 17 amino acid residue segment situated close

C13 to the amino terminus of the predicted GAI protein (SEQ ID NO:2) (Figure 4).

Please replace the paragraph beginning at page 39, line 5, with the following rewritten paragraph:

C14 A previous publication described the isolation, following γ-irradiation mutagenesis, of *gai* derivative alleles[5]. These alleles, when homozygous, confer a tall phenotype indistinguishable from that conferred by GAI[5]. Sequencing of amplified fragments from several of the derivative alleles (*gai-di*, *gai-d2*, *gai-d5* and *gai-d7*) showed that each contains the 51 bp deletion characteristic of *gai*. Nucleotide and encoded amino acid sequences of these alleles are shown in Figure 6 (SEQ ID NOS:3 to SEQ ID NO:10). They also contain additional mutations that could confer a non-functional gene product (Table 1). The fact that loss of *gai* mutant phenotype is correlated with each of these mutations, together with the reversion data (see above), confirms that *GAI* has been cloned. Furthermore, these results are consistent with predictions that the *gai-d* alleles would be null alleles[5,6].